

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
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Application Serial Number: 10/559,825  
Source: IFWP  
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IFWP

**RAW SEQUENCE LISTING**

DATE: 12/16/2005

PATENT APPLICATION: US/10/559,825

TIME: 15:33:38

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\12162005\J559825.raw

```

3 <110> APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
4     REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
5     HUMAN SERVICES
6     Schneerson, Rachel
7     Leppla, Stephen H.
8     Robbins, John B.
9     Shiloach, Joseph
10    Kubler-Kielb, Joanna
11    Liu, Darrell
12    Majadly, Fathy
14 <120> TITLE OF INVENTION: GAMMA PGA CONJUGATES FOR ELICITING IMMUNE RESPONSES DIRECTED
15    AGAINST BACILLI
17 <130> FILE REFERENCE: 4239-68226-07
C--> 19 <140> CURRENT APPLICATION NUMBER: US/10/559,825
C--> 19 <141> CURRENT FILING DATE: 2005-12-02
19 <150> PRIOR APPLICATION NUMBER: PCT/US2004/017736
20 <151> PRIOR FILING DATE: 2004-06-04
22 <150> PRIOR APPLICATION NUMBER: US 60/476,598
23 <151> PRIOR FILING DATE: 2003-06-05
25 <160> NUMBER OF SEQ ID NOS: 3
27 <170> SOFTWARE: PatentIn version 3.2
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 13
31 <212> TYPE: PRT
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
35 <223> OTHER INFORMATION: Basic peptide derived from HIV-1 Tat protein.
37 <400> SEQUENCE: 1
39 Gly Arg Lys Lys Arg Arg Gln Arg Arg Pro Pro Gln
40 1          5          10
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 2295
45 <212> TYPE: DNA
46 <213> ORGANISM: Bacillus anthracis
49 <220> FEATURE:
50 <221> NAME/KEY: CDS
51 <222> LOCATION: (1)..(2292)
53 <400> SEQUENCE: 2
54 atg aaa aaa cga aaa gtg tta ata cca tta atg gca ttg tct acg ata      48
55 Met Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile
56 1          5          10          15
58 tta gtt tca agc aca ggt aat tta gag gtg att cag gca gaa gtt aaa      96
59 Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys

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60	20	25	30	
62	cag gag aac cgg tta tta aat gaa tca gaa tca agt tcc cag ggg tta	144		
63	Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu			
64	35 40 45			
66	cta gga tac tat ttt agt gat ttg aat ttt caa gca ccc atg gtg gtt	192		
67	Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val			
68	50 55 60			
70	acc tct tct act aca ggg gat tta tct att cct agt tct gag tta gaa	240		
71	Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu			
72	65 70 75 80			
74	aat att cca tcg gaa aac caa tat ttt caa tct gct att tgg tca gga	288		
75	Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly			
76	85 90 95			
78	ttt atc aaa gtt aag aag agt gat gaa tat aca ttt gct act tcc gct	336		
79	Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala			
80	100 105 110			
82	gat aat cat gta aca atg tgg gta gat gac caa gaa gtg att aat aaa	384		
83	Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys			
84	115 120 125			
86	gct tct aat tct aac aaa atc aga tta gaa aaa gga aga tta tat caa	432		
87	Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln			
88	130 135 140			
90	ata aaa att caa tat caa cga gaa aat cct act gaa aaa gga ttg gat	480		
91	Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp			
92	145 150 155 160			
94	ttc aag ttg tac tgg acc gat tct caa aat aaa aaa gaa gtg att tct	528		
95	Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser			
96	165 170 175			
98	agt gat aac tta caa ttg cca gaa tta aaa caa aaa tct tcg aac tca	576		
99	Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser			
100	180 185 190			
102	aga aaa aag cga agt aca agt gct gga cct acg gtt cca gac cgt gac	624		
103	Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp			
104	195 200 205			
106	aat gat gga atc cct gat tca tta gag gta gaa gga tat acg gtt gat	672		
107	Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp			
108	210 215 220			
110	gtc aaa aat aaa aga act ttt ctt tca cca tgg att tct aat att cat	720		
111	Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His			
112	225 230 235 240			
114	gaa aag aaa gga tta acc aaa tat aaa tca tct cct gaa aaa tgg agc	768		
115	Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser			
116	245 250 255			
118	acg gct tct gat ccg tac agt gat ttc gaa aag gtt aca gga cgg att	816		
119	Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile			
120	260 265 270			
122	gat aag aat gta tca cca gag gca aga cac ccc ctt gtg gca gct tat	864		
123	Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr			
124	275 280 285			

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126	ccg	att	gta	cat	gta	gat	atg	gag	aat	att	att	ctc	tca	aaa	aat	gag	912
127	Pro	Ile	Val	His	Val	Asp	Met	Glu	Asn	Ile	Ile	Leu	Ser	Lys	Asn	Glu	
128		290					295					300					
130	gat	caa	tcc	aca	cag	aat	act	gat	agt	caa	acg	aga	aca	ata	agt	aaa	960
131	Asp	Gln	Ser	Thr	Gln	Asn	Thr	Asp	Ser	Gln	Thr	Arg	Thr	Ile	Ser	Lys	
132	305					310					315				320		
134	aat	act	tct	aca	agt	agg	aca	cat	act	agt	gaa	gta	cat	gga	aat	gca	1008
135	Asn	Thr	Ser	Thr	Ser	Arg	Thr	His	Thr	Ser	Glu	Val	His	Gly	Asn	Ala	
136				325						330					335		
138	gaa	gtg	cat	gcg	tcg	ttc	ttt	gat	att	ggg	ggg	agt	gta	tct	gca	gga	1056
139	Glu	Val	His	Ala	Ser	Phe	Phe	Asp	Ile	Gly	Gly	Ser	Val	Ser	Ala	Gly	
140				340					345					350			
142	ttt	agt	aat	tcg	aat	tca	agt	acg	gtc	gca	att	gat	cat	tca	cta	tct	1104
143	Phe	Ser	Asn	Ser	Asn	Ser	Ser	Thr	Val	Ala	Ile	Asp	His	Ser	Leu	Ser	
144			355					360					365				
146	cta	gca	ggg	gaa	aga	act	tgg	gct	gaa	aca	atg	ggg	tta	aat	acc	gct	1152
147	Leu	Ala	Gly	Glu	Arg	Thr	Trp	Ala	Glu	Thr	Met	Gly	Leu	Asn	Thr	Ala	
148		370					375					380					
150	gat	aca	gca	aga	tta	aat	gcc	aat	att	aga	tat	gta	aat	act	ggg	acg	1200
151	Asp	Thr	Ala	Arg	Leu	Asn	Ala	Asn	Ile	Arg	Tyr	Val	Asn	Thr	Gly	Thr	
152	385					390					395				400		
154	gct	cca	atc	tac	aac	gtg	tta	cca	acg	act	tcg	tta	gtg	tta	gga	aaa	1248
155	Ala	Pro	Ile	Tyr	Asn	Val	Leu	Pro	Thr	Thr	Ser	Leu	Val	Leu	Gly	Lys	
156				405					410					415			
158	aat	caa	aca	ctc	gcg	aca	att	aaa	gct	aag	gaa	aac	caa	tta	agt	caa	1296
159	Asn	Gln	Thr	Leu	Ala	Thr	Ile	Lys	Ala	Lys	Glu	Asn	Gln	Leu	Ser	Gln	
160			420						425					430			
162	ata	ctt	gca	cct	aat	aat	tat	tat	cct	tct	aaa	aac	ttg	gcg	cca	atc	1344
163	Ile	Leu	Ala	Pro	Asn	Asn	Tyr	Tyr	Pro	Ser	Lys	Asn	Leu	Ala	Pro	Ile	
164			435					440					445				
166	gca	tta	aat	gca	caa	gac	gat	ttc	agt	tct	act	cca	att	aca	atg	aat	1392
167	Ala	Leu	Asn	Ala	Gln	Asp	Asp	Phe	Ser	Ser	Thr	Pro	Ile	Thr	Met	Asn	
168		450				455					460						
170	tac	aat	caa	ttt	ctt	gag	tta	gaa	aaa	acg	aaa	caa	tta	aga	tta	gat	1440
171	Tyr	Asn	Gln	Phe	Leu	Glu	Leu	Glu	Lys	Thr	Lys	Gln	Leu	Arg	Leu	Asp	
172	465					470					475				480		
174	acg	gat	caa	gta	tat	ggg	aat	ata	gca	aca	tac	aat	ttt	gaa	aat	gga	1488
175	Thr	Asp	Gln	Val	Tyr	Gly	Asn	Ile	Ala	Thr	Tyr	Asn	Phe	Glu	Asn	Gly	
176				485					490					495			
178	aga	gtg	agg	gtg	gat	aca	ggc	tcg	aac	tgg	agt	gaa	gtg	tta	ccg	caa	1536
179	Arg	Val	Arg	Val	Asp	Thr	Gly	Ser	Asn	Trp	Ser	Glu	Val	Leu	Pro	Gln	
180			500						505					510			
182	att	caa	gaa	aca	act	gca	cgt	atc	att	ttt	aat	gga	aaa	gat	tta	aat	1584
183	Ile	Gln	Glu	Thr	Thr	Ala	Arg	Ile	Ile	Phe	Asn	Gly	Lys	Asp	Leu	Asn	
184			515					520					525				
186	ctg	gta	gaa	agg	cgg	ata	gcg	gcg	ggt	aat	cct	agt	gat	cca	tta	gaa	1632
187	Leu	Val	Glu	Arg	Arg	Ile	Ala	Ala	Val	Asn	Pro	Ser	Asp	Pro	Leu	Glu	
188		530					535					540					
190	acg	act	aaa	ccg	gat	atg	aca	tta	aaa	gaa	gcc	ctt	aaa	ata	gca	ttt	1680

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191 Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe
192 545                    550                    555                    560
194 gga ttt aac gaa ccg aat gga aac tta caa tat caa ggg aaa gac ata      1728
195 Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile
196                    565                    570                    575
198 acc gaa ttt gat ttt aat ttc gat caa caa aca tct caa aat atc aag      1776
199 Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys
200                    580                    585                    590
202 aat cag tta gcg gaa tta aac gca act aac ata tat act gta tta gat      1824
203 Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp
204                    595                    600                    605
206 aaa atc aaa tta aat gca aaa atg aat att tta ata aga gat aaa cgt      1872
207 Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg
208        610                    615                    620
210 ttt cat tat gat aga aat aac ata gca gtt ggg gcg gat gag tca gta      1920
211 Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val
212 625                    630                    635                    640
214 gtt aag gag gct cat aga gaa gta att aat tcg tca aca gag gga tta      1968
215 Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu
216                    645                    650                    655
218 ttg tta aat att gat aag gat ata aga aaa ata tta tca ggt tat att      2016
219 Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile
220                    660                    665                    670
222 gta gaa att gaa gat act gaa ggg ctt aaa gaa gtt ata aat gac aga      2064
223 Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg
224                    675                    680                    685
226 tat gat atg ttg aat att tct agt tta cgg caa gat gga aaa aca ttt      2112
227 Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe
228        690                    695                    700
230 ata gat ttt aaa aaa tat aat gat aaa tta ccg tta tat ata agt aat      2160
231 Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn
232 705                    710                    715                    720
234 ccc aat tat aag gta aat gta tat gct gtt act aaa gaa aac act att      2208
235 Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile
236                    725                    730                    735
238 att aat cct agt gag aat ggg gat act agt acc aac ggg atc aag aaa      2256
239 Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys
240                    740                    745                    750
242 att tta atc ttt tct aaa aaa ggc tat gag ata gga taa      2295
243 Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
244        755                    760
247 <210> SEQ ID NO: 3
248 <211> LENGTH: 764
249 <212> TYPE: PRT
250 <213> ORGANISM: Bacillus anthracis
252 <400> SEQUENCE: 3
254 Met Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile
255 1                    5                    10                    15
258 Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys

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259          20          25          30
262 Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu
263          35          40          45
266 Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val
267          50          55          60
270 Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu
271 65          70          75          80
274 Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly
275          85          90          95
278 Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala
279          100          105          110
282 Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys
283          115          120          125
286 Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln
287          130          135          140
290 Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp
291 145          150          155          160
294 Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser
295          165          170          175
298 Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser
299          180          185          190
302 Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp
303          195          200          205
306 Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp
307          210          215          220
310 Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His
311 225          230          235          240
314 Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser
315          245          250          255
318 Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile
319          260          265          270
322 Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr
323          275          280          285
326 Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu
327          290          295          300
330 Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys
331 305          310          315          320
334 Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala
335          325          330          335
338 Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly
339          340          345          350
342 Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser
343          355          360          365
346 Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala
347          370          375          380
350 Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr
351 385          390          395          400
354 Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys
355          405          410          415

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VERIFICATION SUMMARY

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L:19 M:270 C: Current Application Number differs, Replaced Current Application No

L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date